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OM protein - protein search, using sw model

Run on: August 23, 2007, 12:57:35 ; Search time 210 Seconds
                                            (without alignments)
                                            27.962 Million cell updates/sec

Title: US-10-531-701-18
Perfect score: 72
Sequence: 1 CSSVTAWTTGCG 12

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 1139688

Minimum DB seq length: 5
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   A_Geneseq_200701:*
                1: geneseqp1980s:*
                2: geneseqp1990s:*
                3: geneseqp2000s:*
                4: geneseqp2001s:*
                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*
                10: geneseqp2006s:*
                11: geneseqp2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	72	100.0	12	8	ADO85937	Ado85937 Cyclic po
2	41	56.9	12	8	ADO85941	Ado85941 Cyclic po
3	40	55.6	24	2	AAY09276	Aay09276 Antifreez
4	39	54.2	12	8	ADO85940	Ado85940 Cyclic po
5	38	52.8	9	5	AAU92600	Aau92600 PHOR1-F5D
6	38	52.8	9	5	AAU92399	Aau92399 PHOR1-F5D

7	38	52.8	9	5	AAU92809	Aau92809 PHOR1-F5D
8	38	52.8	10	5	AAU92956	Aau92956 PHOR1-F5D
9	38	52.8	10	5	AAU92653	Aau92653 PHOR1-F5D
10	38	52.8	10	5	AAU92816	Aau92816 PHOR1-F5D
11	38	52.8	25	4	AAB75264	Aab75264 Human sec
12	37	51.4	9	5	AAU92793	Aau92793 PHOR1-F5D
13	37	51.4	10	5	AAU92959	Aau92959 PHOR1-F5D
14	37	51.4	10	5	AAU92838	Aau92838 PHOR1-F5D
15	36.5	50.7	18	10	AEJ08867	Aej08867 Phage fd-
16	36	50.0	12	9	ADY41213	Ady41213 Human gua
17	36	50.0	12	9	ADY40991	Ady40991 Human gua
18	36	50.0	12	9	ADY41037	Ady41037 Human gua
19	36	50.0	12	9	AEB80440	Aeb80440 Human gua
20	36	50.0	12	9	AEB80662	Aeb80662 Human gua
21	36	50.0	12	9	AEB80486	Aeb80486 Human gua
22	36	50.0	12	10	AEK69806	Aek69806 Chymotryp
23	36	50.0	12	10	AEK70028	Aek70028 Chymotryp
24	36	50.0	12	10	AEK69852	Aek69852 Chymotryp
25	36	50.0	13	9	ADY41338	Ady41338 Human gua
26	36	50.0	13	9	ADY41162	Ady41162 Human gua
27	36	50.0	13	9	ADY41468	Ady41468 Human gua
28	36	50.0	13	9	AEB80787	Aeb80787 Human gua
29	36	50.0	13	9	AEB80917	Aeb80917 Human gua
30	36	50.0	13	9	AEB80611	Aeb80611 Human gua
31	36	50.0	13	10	AEK70153	Aek70153 Chymotryp
32	36	50.0	13	10	AEK70283	Aek70283 Chymotryp
33	36	50.0	13	10	AEK69977	Aek69977 Chymotryp
34	36	50.0	14	9	ADY41722	Ady41722 Human gua
35	36	50.0	14	9	AEB81171	Aeb81171 Human gua
36	36	50.0	14	10	AEK70537	Aek70537 Chymotryp
37	36	50.0	17	2	AAR06081	Aar06081 Immunorea
38	36	50.0	26	6	ABJ19716	Abj19716 Human sec
39	36	50.0	26	6	ABP99743	Abp99743 Human sec
40	36	50.0	26	6	ABR01234	Abr01234 Human gen
41	36	50.0	26	6	ADA98331	Ada98331 Human sec
42	36	50.0	27	3	AAB39404	Aab39404 Human sec
43	35	48.6	12	6	ABR75736	Abr75736 Liver res
44	35	48.6	12	7	ADN07316	Adn07316 Liver res
45	35	48.6	25	5	ABG62949	Abg62949 Ligand/re
46	35	48.6	25	5	ABG62951	Abg62951 Ligand/re
47	35	48.6	25	5	ABG62952	Abg62952 Ligand/re
48	35	48.6	25	5	ABG62950	Abg62950 Ligand/re
49	35	48.6	25	8	ADM74130	Adm74130 Ligand/re
50	35	48.6	25	8	ADM74131	Adm74131 Ligand/re
51	35	48.6	25	8	ADM74134	Adm74134 Ligand/re
52	35	48.6	25	8	ADM74135	Adm74135 Ligand/re
53	35	48.6	27	5	ABG62946	Abg62946 Ligand/re
54	35	48.6	27	5	ABG62947	Abg62947 Ligand/re
55	35	48.6	27	5	ABG62945	Abg62945 Ligand/re
56	35	48.6	27	5	ABG62948	Abg62948 Ligand/re
57	35	48.6	27	8	ADM74128	Adm74128 Ligand/re
58	35	48.6	27	8	ADM74129	Adm74129 Ligand/re
59	35	48.6	27	8	ADM74133	Adm74133 Ligand/re
60	35	48.6	27	8	ADM74132	Adm74132 Ligand/re
61	35	48.6	27	9	ADZ47462	Adz47462 Human HAS
62	34	47.2	8	8	ADJ66046	Adj66046 Human som
63	34	47.2	21	10	AEH44929	Aeh44929 IL-17 Zcy

ID   ADO85937 standard; peptide; 12 AA.

XX

AC   ADO85937;

XX

DT   29-JUL-2004   (first entry)

XX

DE   Cyclic poly-alpha2,8-sialic acid (PSA) mimetic peptide p65 SeqID 18.

XX

KW   B epitope; poly-alpha2,8-sialic acid; PSA; neural cell adhesion molecule;
KW   NCAM; neurodegenerative disease; brain lesion; spine lesion;
KW   age-related learning problem; memory problem; cancer; peptide therapy;
KW   neuroprotective; cytostatic; mimetic; cyclic.

XX

OS   Synthetic.

XX

FH   Key   Location/Qualifiers
FT   Disulfide-bond 1. .11
FT   /note = Disulphide bond cyclises peptide

XX

PN   EP1411061-A1.

XX

PD   21-APR-2004.

XX

PF   16-OCT-2002; 2002EP-00292548.

XX

PR   16-OCT-2002; 2002EP-00292548.

XX

PA   (CNRS) CNRS CENT NAT RECH SCI.
PA   (UYAI-) UNIV AIX-MARSEILLE II.
PA   (SCHA/) SCHAFER N.
PA   (UYHA-) UNIV HAMBURG.

XX

DR   WPI; 2004-319104/30.

XX

PT   New poly-alpha2,9-sialic acid peptide mimetics comprising a B epitope
PT   recognized by an antipoly-alpha2,8 sialic acid antibody, useful for
PT   treating and/or preventing e.g. neurodegenerative diseases or cancer.

XX

PS   Claim 3; SEQ ID NO 18; 36pp; English.

XX

CC   This invention relates to novel peptides that comprise a B epitope
CC   recognised by an anti-poly-alpha2,8-sialic acid (PSA) antibody.
CC   Specifically, it refers to PSA mimetic peptides that can negatively
CC   regulate cell surface interactions and hence modulate PSA-dependent
CC   neural cell adhesion molecule (NCAM) functions both in vitro and in vivo.
CC   The present invention describes these peptides or derived complexes
CC   thereof as useful in the preparation of a medicament for treating and/ or
CC   preventing a pathological condition including a neurodegenerative
CC   disease, brain and spine lesions, age-related learning and memory
CC   problems, as well as cancer. The peptide may also be used as a
CC   complementary tool to uncover mechanisms of action and unknown functions
CC   of the carbohydrate PSA. Accordingly, such pharmaceutical compositions
CC   can be used appropriately in peptide therapy and exhibit neuroprotective
CC   and cytostatic activities. This peptide sequence is a cyclic PSA mimetic
CC   peptide of the invention.

XX
SQ   Sequence 12 AA;

   Query Match   100.0%;   Score 72;   DB 8;   Length 12;
   Best Local Similarity   100.0%;   Pred. No. 0.0027;
   Matches   12; Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 CSSVTAWTTGCG 12
              ||||||||||||
Db   1 CSSVTAWTTGCG 12

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OM protein - protein search, using sw model

Run on: August 23, 2007, 12:57:49 ; Search time 339 Seconds
                                            (without alignments)
                                            37.951 Million cell updates/sec

Title: US-10-531-701-18
Perfect score: 72
Sequence: 1 CSSVTAWTTGCG 12

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 41180

Minimum DB seq length: 5
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   UniProt_8.4:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	47.2	26	2	Q9TR94_SHEEP	Q9tr94 ovis aries
2	32	44.4	26	2	Q79DW7_AZOVI	Q79dw7 azotobacter
3	32	44.4	29	1	VARF_VIOAR	P58451 viola arven
4	31	43.1	30	2	Q3A9Y9_CARHZ	Q3a9y9 carboxydoth
5	30	41.7	22	2	Q93UU5_ECO57	Q93uu5 escherichia
6	30	41.7	25	2	Q865G5_HYLSY	Q865g5 hylobates s
7	30	41.7	27	1	CXO6A_CONRA	P58914 conus radia
8	29	40.3	21	1	ALL7_OLEEU	P81430 olea europa
9	29	40.3	24	2	Q4XAU4_PLACH	Q4xau4 plasmodium
10	29	40.3	25	1	MT_AGABI	P04358 agaricus bi
11	28	38.9	18	2	Q9ZG65_CHLTR	Q9zg65 chlamydia t
12	28	38.9	20	2	Q9UDF5_HUMAN	Q9udf5 homo sapien
13	28	38.9	27	2	Q6WYW0_9PERC	Q6wyw0 luvarus imp
14	28	38.9	27	2	Q6WYV8_9PERC	Q6wyv8 paracanthur
15	28	38.9	27	2	Q6WYV3_9PERC	Q6wyv3 acanthurus

16	28	38.9	27	2	Q6WYV1_9PERC	Q6wyv1	acanthurus
17	28	38.9	27	2	Q6WYU4_9PERC	Q6wyu4	ctenochaetu
18	28	38.9	27	2	Q6WYU5_9PERC	Q6wyu5	acanthurus
19	28	38.9	27	2	Q6WYU8_9PERC	Q6wyu8	acanthurus
20	28	38.9	27	2	Q6WYT2_9PERC	Q6wyt2	naso macula
21	28	38.9	27	2	Q6WYT9_9PERC	Q6wyt9	naso caerul
22	28	38.9	27	2	Q6WYU9_9PERC	Q6wyu9	acanthurus
23	28	38.9	27	2	Q6WYT7_9PERC	Q6wyt7	naso elegan
24	28	38.9	27	2	Q6WYS5_9PERC	Q6wys5	naso unicor
25	28	38.9	27	2	Q6WYV2_9PERC	Q6wyv2	acanthurus
26	28	38.9	27	2	Q6WYT5_9PERC	Q6wyt5	naso hexaca
27	28	38.9	27	2	Q6WYS8_9PERC	Q6wys8	naso thynno
28	28	38.9	27	2	Q6WYV9_9PERC	Q6wyv9	zanclus cor
29	28	38.9	27	2	Q6WYV7_9PERC	Q6wyv7	prionurus m
30	28	38.9	27	2	Q6WYV0_9PERC	Q6wyv0	acanthurus
31	28	38.9	27	2	Q6WYU1_9PERC	Q6wyu1	naso brachy
32	28	38.9	27	2	Q6WYT1_9PERC	Q6wyt1	naso mcdade
33	28	38.9	27	2	Q6WYT3_9PERC	Q6wyt3	naso lopezi
34	28	38.9	27	2	Q6WYT4_9PERC	Q6wyt4	naso litura
35	28	38.9	27	2	Q6WYT8_9PERC	Q6wyt8	naso caesiu
36	28	38.9	27	2	Q6WYT0_9PERC	Q6wyt0	naso minor.
37	28	38.9	27	2	Q6WYU2_9PERC	Q6wyu2	naso annula
38	28	38.9	27	2	Q6WYS4_9PERC	Q6wys4	naso vlamin
39	28	38.9	27	2	Q6WYT6_9PERC	Q6wyt6	naso fageni
40	28	38.9	27	2	Q6WYS3_9PERC	Q6wys3	naso sp. 1-
41	28	38.9	27	2	Q6WYU3_9PERC	Q6wyu3	ctenochaetu
42	28	38.9	27	2	Q6WYU0_9PERC	Q6wyu0	naso brevir
43	28	38.9	27	2	Q6WYS7_9PERC	Q6wys7	naso tongan
44	28	38.9	27	2	Q6WYV4_9PERC	Q6wyv4	zebrasoma v
45	28	38.9	27	2	Q6WYV6_9PERC	Q6wyv6	prionurus s
46	28	38.9	27	2	Q6WYU7_9PERC	Q6wyu7	acanthurus
47	28	38.9	27	2	Q6WYS9_9PERC	Q6wys9	naso reticu
48	28	38.9	27	2	Q6WYU6_9PERC	Q6wyu6	acanthurus
49	28	38.9	27	2	Q6WYS6_9PERC	Q6wys6	naso tubero
50	28	38.9	28	2	Q4X2U3_PLACH	Q4x2u3	plasmodium
51	28	38.9	29	2	Q9N1W3_HORSE	Q9n1w3	equus cabal
52	27	37.5	16	2	Q3ZEV7_9CHAR	Q3zev7	tringa stag
53	27	37.5	23	2	Q9R2G4_KLEPN	Q9r2g4	klebsiella
54	27	37.5	27	2	Q9MKR2_MELGA	Q9mkr2	meleagris g
55	27	37.5	27	2	Q45UI9_9HIV1	Q45ui9	human immun
56	27	37.5	27	2	Q45UI5_9HIV1	Q45ui5	human immun
57	27	37.5	27	2	Q45UI6_9HIV1	Q45ui6	human immun
58	27	37.5	27	2	Q45UI8_9HIV1	Q45ui8	human immun
59	27	37.5	27	2	Q45UI7_9HIV1	Q45ui7	human immun
60	27	37.5	28	2	Q5EMT0_MAGGR	Q5emt0	magnaporthe
61	27	37.5	28	2	Q4RCL2_TETNG	Q4rcl2	tetraodon n
62	26	36.1	11	2	Q99JC3_9MURI	Q99jc3	rattus sp.
63	26	36.1	16	2	Q8HUM0_9MAGN	Q8hum0	eudicot env
64	26	36.1	16	2	Q8HUM1_9POAL	Q8hum1	uncultured
65	26	36.1	19	2	Q41567_WHEAT	Q41567	triticum ae
66	26	36.1	20	1	NLTP1_HELAN	P82007	helianthus
67	26	36.1	21	2	Q8MJP1_CALJA	Q8mjp1	callithrix
68	26	36.1	21	2	Q8MJP4_SAGFU	Q8mjp4	saguinus fu
69	26	36.1	21	2	Q8MJP0_CEBPY	Q8mjp0	cebuella py
70	26	36.1	24	2	Q7M1P2_HELAN	Q7m1p2	helianthus
71	26	36.1	25	2	Q23QB2_TETTH	Q23qb2	tetrahymena
72	26	36.1	26	2	Q2HWU6_DROSE	Q2hwu6	drosophila

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OM protein - protein search, using sw model

Run on: August 23, 2007, 13:01:39 ; Search time 38 Seconds
                                                (without alignments)
                                                30.384 Million cell updates/sec

Title: US-10-531-701-18
Perfect score: 72
Sequence: 1 CSSVTAWTTGCG 12

Scoring table: BLOSUM62
                     Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 6197

Minimum DB seq length: 5
Maximum DB seq length: 30

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   PIR_80:*
                     1: pir1:*
                     2: pir2:*
                     3: pir3:*
                     4: pir4:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	34	47.2	19	2	S57515	T cell receptor be
2	33	45.8	19	2	S57516	T cell receptor be
3	33	45.8	25	2	B44908	chitinase (EC 3.2.
4	30	41.7	20	2	PH1358	Ig heavy chain DJ
5	30	41.7	22	2	PT0303	Ig heavy chain CDR
6	30	41.7	28	2	PH1363	Ig heavy chain DJ
7	29	40.3	17	2	PH1331	Ig heavy chain DJ
8	29	40.3	25	1	SMMR	metallothionein -
9	28	38.9	19	2	PH1352	Ig heavy chain DJ
10	28	38.9	19	2	PH1315	Ig heavy chain DJ
11	27	37.5	23	2	A43872	fimbrial adhesin C
12	26	36.1	23	2	S07967	T-cell receptor be
13	26	36.1	24	2	PH0084	fatty acid-binding

14	26	36.1	25	2	S71387	alpha-2-macroglobu
15	26	36.1	28	2	I52627	erythrocyte chemok
16	25	34.7	20	2	S66222	defensin AMP2 - Da
17	25	34.7	21	2	S28436	major outer membra
18	25	34.7	22	2	A35418	brain natriuretic
19	25	34.7	25	2	A49389	alkaline serine pr
20	25	34.7	28	2	S07826	venom protein - Am
21	25	34.7	29	2	S58388	T-cell receptor be
22	25	34.7	30	1	SNUMP	sillucin - Rhizomu
23	25	34.7	30	2	S05223	photosystem I 6.5K
24	25	34.7	30	2	H97596	hypothetical prote
25	24	33.3	11	2	S66196	alcohol dehydrogen
26	24	33.3	14	2	PH0747	T-cell receptor be
27	24	33.3	15	2	PH0750	T-cell receptor be
28	24	33.3	26	2	S55029	CAP3 protein - ant
29	24	33.3	26	2	A58955	metalloendoprotein
30	24	33.3	27	2	T06375	probable ferredoxi
31	24	33.3	27	2	S77649	hypothetical prote
32	24	33.3	29	2	PH0259	T-cell receptor Vb
33	24	33.3	29	2	A56283	kalata B1 [validat
34	23.5	32.6	20	2	S38763	S-adenosyl-L-methi
35	23	31.9	13	2	B26406	Ig kappa chain J r
36	23	31.9	13	2	A47630	Ig kappa chain J r
37	23	31.9	18	2	S19914	choline O-acetyltr
38	23	31.9	19	2	A44379	alpha-conotoxin SI
39	23	31.9	22	2	B26212	carboxypeptidase B
40	23	31.9	22	2	S42567	cytochrome-b5 redu
41	23	31.9	26	1	SMNC	metallothionein -
42	23	31.9	28	2	C35948	phospholipase A2 (
43	23	31.9	29	2	B43620	omega-conotoxin GV
44	23	31.9	30	2	S68639	nigroxin A - black
45	23	31.9	30	2	S68640	nigroxin B - black
46	22	30.6	9	2	S07241	litorin - Rohde's
47	22	30.6	10	2	T17057	cytochrome-c oxida
48	22	30.6	10	2	T12303	cytochrome-c oxida
49	22	30.6	10	2	T17060	cytochrome-c oxida
50	22	30.6	10	2	T17072	cytochrome-c oxida
51	22	30.6	12	2	PH1675	Ig heavy chain V r
52	22	30.6	13	2	PH1676	Ig heavy chain V r
53	22	30.6	14	2	PH1677	Ig heavy chain V r
54	22	30.6	15	2	PH0751	T-cell receptor be
55	22	30.6	17	2	I67524	CD33 antigen homol
56	22	30.6	18	2	S23971	alpha-macroglobuli
57	22	30.6	19	2	G49048	T-cell receptor be
58	22	30.6	20	2	T46626	hypothetical prote
59	22	30.6	21	2	PH1690	Ig heavy chain V r
60	22	30.6	21	2	PH1688	Ig heavy chain V r
61	22	30.6	22	2	PH1680	Ig heavy chain V r
62	22	30.6	22	2	PH1679	Ig heavy chain V r
63	22	30.6	22	2	PH1678	Ig heavy chain V r
64	22	30.6	23	2	PH1689	Ig heavy chain V r
65	22	30.6	23	2	PH1694	Ig heavy chain V r
66	22	30.6	23	2	PH1695	Ig heavy chain V r
67	22	30.6	23	2	PH1693	Ig heavy chain V r
68	22	30.6	23	2	PH1681	Ig heavy chain V r
69	22	30.6	23	2	PH1682	Ig heavy chain V r
70	22	30.6	23	2	PH1691	Ig heavy chain V r

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:06 ; Search time 69 Seconds
                                             (without alignments)
                                             163.111 Million cell updates/sec

Title: SEQ18-SEQ18
Perfect score: 138
Sequence: 1 CSSVTAWTTGcCSSVTAWTTGcg 23

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   A_Geneseq_200701:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*
                 10: geneseqp2006s:*
                 11: geneseqp2007s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
     1   72   52.2   12   8   ADO85937   Ado85937 Cyclic po
     2   72   52.2   753   8   ADP30988   Adp30988 Human sec
     3   72   52.2   1861 10   AEI57987   Aei57987 Thale cre
     4   69   50.0   1509 10   AEI57371   Aei57371 Thale cre
     5   69   50.0   1510 10   AEI56371   Aei56371 Thale cre
     6   69   50.0   1600 10   AEI56169   Aei56169 Zea mays

7	69	50.0	1847	10	AEI58385	Aei58385 Zea mays
8	68.5	49.6	1396	10	AEI55999	Aei55999 Thale cre
9	68	49.3	1432	10	AEI56479	Aei56479 Zea mays
10	68	49.3	1440	10	AEI57593	Aei57593 Thale cre
11	68	49.3	1965	10	AEI56625	Aei56625 Zea mays
12	68	49.3	2280	10	AEI57411	Aei57411 Thale cre
13	68	49.3	2487	10	AEI57141	Aei57141 Thale cre
14	68	49.3	2616	9	AEB49675	Aeb49675 N. mening
15	67.5	48.9	1434	10	AEI56727	Aei56727 Zea mays
16	67	48.6	1577	10	AEI56651	Aei56651 Zea mays
17	66	47.8	762	8	ADP31012	Adp31012 Human sec
18	66	47.8	824	10	AEI56575	Aei56575 Zea mays
19	66	47.8	885	8	ADP31011	Adp31011 Human sec
20	66	47.8	1537	10	AEI56249	Aei56249 Zea mays
21	66	47.8	1568	10	AEI58079	Aei58079 Thale cre
22	66	47.8	1595	10	AEI57633	Aei57633 Thale cre
23	66	47.8	1696	10	AEI56163	Aei56163 Zea mays
24	66	47.8	1951	10	AEI58651	Aei58651 Soybean p
25	66	47.8	2268	10	AEI57595	Aei57595 Thale cre
26	66	47.8	2328	10	AEI57469	Aei57469 Thale cre
27	66	47.8	2484	8	ADP66690	Adp66690 Human mis
28	65.5	47.5	1092	8	ADP31153	Adp31153 Human sec
29	65	47.1	1305	10	AEI57293	Aei57293 Thale cre
30	65	47.1	1324	10	AEI58241	Aei58241 Thale cre
31	65	47.1	1401	10	AEI56871	Aei56871 Thale cre
32	65	47.1	1527	10	AEI56859	Aei56859 Thale cre
33	65	47.1	1602	10	AEI56221	Aei56221 Zea mays
34	65	47.1	1623	10	AEI57045	Aei57045 Thale cre
35	65	47.1	2017	10	AEI58215	Aei58215 Zea mays
36	65	47.1	2119	10	AEI60331	Aei60331 Bread whe
37	65	47.1	2380	10	AEI57231	Aei57231 Thale cre
38	65	47.1	2499	10	AEI55671	Aei55671 Thale cre
39	65	47.1	2762	10	AEI58209	Aei58209 Thale cre
40	65	47.1	3331	10	AEI57107	Aei57107 Thale cre
41	64.5	46.7	1069	10	AEI56761	Aei56761 Zea mays
42	64.5	46.7	1357	10	AEI57257	Aei57257 Thale cre
43	64.5	46.7	1359	10	AEI56507	Aei56507 Thale cre
44	64.5	46.7	1566	10	AEI55755	Aei55755 Thale cre
45	64.5	46.7	1855	10	AEI58011	Aei58011 Thale cre
46	64.5	46.7	1856	10	AEI55855	Aei55855 Thale cre
47	64	46.4	240	8	ADP31579	Adp31579 Human sec
48	64	46.4	619	10	AEI56055	Aei56055 Zea mays
49	64	46.4	1002	8	ADP30866	Adp30866 Human sec
50	64	46.4	1117	10	AEI56991	Aei56991 Thale cre
51	64	46.4	1170	8	ADP30919	Adp30919 Human sec
52	64	46.4	1170	8	ADP30922	Adp30922 Human sec
53	64	46.4	1194	10	AEI57861	Aei57861 Thale cre
54	64	46.4	1293	10	AEI58071	Aei58071 Thale cre
55	64	46.4	1293	10	AEI57643	Aei57643 Thale cre
56	64	46.4	1407	10	AEI55655	Aei55655 Thale cre
57	64	46.4	1419	10	AEI55665	Aei55665 Thale cre
58	64	46.4	1435	10	AEI60567	Aei60567 Soybean p
59	64	46.4	1490	10	AEI58067	Aei58067 Thale cre
60	64	46.4	1676	10	AEI56079	Aei56079 Zea mays
61	64	46.4	1682	10	AEI57991	Aei57991 Thale cre
62	64	46.4	1691	10	AEI56295	Aei56295 Zea mays
63	64	46.4	2458	10	AEI57027	Aei57027 Thale cre

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:06 ; Search time 69 Seconds
                                              (without alignments)
                                              163.111 Million cell updates/sec

Title: SEQ18-SEQ22
Perfect score: 132
Sequence: 1 CSSVTAWTTGCCSKIASMETGCG 23

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   A_Geneseq_200701:*
                  1: geneseqp1980s:*
                  2: geneseqp1990s:*
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                  6: geneseqp2003as:*
                  7: geneseqp2003bs:*
                  8: geneseqp2004s:*
                  9: geneseqp2005s:*
                  10: geneseqp2006s:*
                  11: geneseqp2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB   ID   Description
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        1   67   50.8   3723 10   AEI58335   Aei58335 Zea mays
        2   66   50.0   12   8   ADO85941   Ado85941 Cyclic po
        3   66   50.0   12   8   ADO85937   Ado85937 Cyclic po
        4   66   50.0   1509 10   AEI57371   Aei57371 Thale cre
        5   66   50.0   1510 10   AEI56371   Aei56371 Thale cre
        6   64   48.5   1568 10   AEI58079   Aei58079 Thale cre

7	64	48.5	1595	10	AEI57633	Aei57633 Thale cre
8	62	47.0	152	8	ADY06675	Ady06675 Plant ful
9	62	47.0	882	8	ADP31688	Adp31688 Human sec
10	61	46.2	1269	8	ADU23456	Adu23456 Sulfolobu
11	61	46.2	1704	10	AEI56537	Aei56537 Thale cre
12	61	46.2	1861	10	AEI57987	Aei57987 Thale cre
13	60.5	45.8	893	10	AEI57475	Aei57475 Thale cre
14	60.5	45.8	1092	8	ADP31153	Adp31153 Human sec
15	60	45.5	753	8	ADP30988	Adp30988 Human sec
16	60	45.5	1422	10	AEI56223	Aei56223 Zea mays
17	60	45.5	1435	10	AEI60567	Aei60567 Soybean p
18	60	45.5	1691	10	AEI56295	Aei56295 Zea mays
19	60	45.5	1711	10	AEI57723	Aei57723 Zea mays
20	60	45.5	1833	8	ADP30642	Adp30642 Human sec
21	60	45.5	2344	10	AEI57029	Aei57029 Thale cre
22	59	44.7	12	8	ADO85940	Ado85940 Cyclic po
23	59	44.7	1407	10	AEI55655	Aei55655 Thale cre
24	59	44.7	1440	10	AEI57593	Aei57593 Thale cre
25	59	44.7	1616	8	ADP31004	Adp31004 Human sec
26	59	44.7	1616	8	ADP30987	Adp30987 Human sec
27	59	44.7	1616	8	ADP30967	Adp30967 Human sec
28	59	44.7	1682	10	AEI57991	Aei57991 Thale cre
29	59	44.7	1806	10	AEI56405	Aei56405 Zea mays
30	59	44.7	1848	10	AEI56905	Aei56905 Zea mays
31	58.5	44.3	1818	10	AEI56265	Aei56265 Zea mays
32	58	43.9	672	8	ADP30498	Adp30498 Human sec
33	58	43.9	1401	8	ADP30532	Adp30532 Human sec
34	58	43.9	1401	10	AEI56871	Aei56871 Thale cre
35	58	43.9	1420	8	ADP30944	Adp30944 Human sec
36	58	43.9	1470	8	ADP31290	Adp31290 Human sec
37	58	43.9	1638	10	AEI56193	Aei56193 Zea mays
38	58	43.9	2280	10	AEI57411	Aei57411 Thale cre
39	58	43.9	2380	10	AEI57231	Aei57231 Thale cre
40	58	43.9	2487	10	AEI57141	Aei57141 Thale cre
41	58	43.9	2628	10	AEI58225	Aei58225 Zea mays
42	58	43.9	3331	10	AEI57107	Aei57107 Thale cre
43	57.5	43.6	484	8	ADP31628	Adp31628 Human sec
44	57.5	43.6	583	8	ADP30553	Adp30553 Human sec
45	57.5	43.6	1419	10	AEI55665	Aei55665 Thale cre
46	57.5	43.6	1462	10	AEI56707	Aei56707 Zea mays
47	57.5	43.6	1490	10	AEI58067	Aei58067 Thale cre
48	57.5	43.6	1750	10	AEI56103	Aei56103 Thale cre
49	57.5	43.6	1751	10	AEI57959	Aei57959 Thale cre
50	57.5	43.6	1869	10	AEI57877	Aei57877 Thale cre
51	57	43.2	501	8	ADP31689	Adp31689 Human sec
52	57	43.2	507	8	ADP30869	Adp30869 Human sec
53	57	43.2	856	8	ADP30972	Adp30972 Human sec
54	57	43.2	1195	10	AEI57953	Aei57953 Thale cre
55	57	43.2	1199	10	AEI55925	Aei55925 Thale cre
56	57	43.2	1215	8	ADP30898	Adp30898 Human sec
57	57	43.2	1215	8	ADP30900	Adp30900 Human sec
58	57	43.2	1231	10	AEI57495	Aei57495 Thale cre
59	57	43.2	1248	8	ADP31346	Adp31346 Human sec
60	57	43.2	1337	10	AEI56893	Aei56893 Thale cre
61	57	43.2	1371	10	AEI57113	Aei57113 Thale cre
62	57	43.2	1383	10	AEI57315	Aei57315 Thale cre
63	57	43.2	1533	10	AEI57589	Aei57589 Thale cre

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:06 ; Search time 69 Seconds
                                              (without alignments)
                                              163.111 Million cell updates/sec

Title: SEQ22-SEQ18
Perfect score: 132
Sequence: 1 CSKIASMETGCCSSVTAWTTGCG 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   A_Geneseq_200701:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
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                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*
                 10: geneseqp2006s:*
                 11: geneseqp2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	72	54.5	12	8	ADO85937	Ado85937 Cyclic po
2	64	48.5	1396	10	AEI55999	Aei55999 Thale cre
3	63	47.7	753	8	ADP30988	Adp30988 Human sec
4	62.5	47.3	1691	10	AEI56295	Aei56295 Zea mays
5	62	47.0	2280	10	AEI57411	Aei57411 Thale cre
6	62	47.0	2487	10	AEI57141	Aei57141 Thale cre

7	61.5	46.6	1951	10	AEI58651	Aei58651	Soybean p
8	61	46.2	2604	10	AEI57169	Aei57169	Thale cre
9	61	46.2	3723	10	AEI58335	Aei58335	Zea mays
10	60	45.5	12	8	ADO85941	Ado85941	Cyclic po
11	60	45.5	1209	10	AEI59917	Aei59917	Bread whe
12	60	45.5	1965	10	AEI56625	Aei56625	Zea mays
13	60	45.5	2499	10	AEI55671	Aei55671	Thale cre
14	60	45.5	2773	10	AEI56999	Aei56999	Thale cre
15	60	45.5	2791	10	AEI58359	Aei58359	Thale cre
16	60	45.5	3060	10	AEI57065	Aei57065	Thale cre
17	59.5	45.1	1069	10	AEI56761	Aei56761	Zea mays
18	59.5	45.1	1446	10	AEI56195	Aei56195	Zea mays
19	59.5	45.1	1833	8	ADP30642	Adp30642	Human sec
20	59	44.7	619	10	AEI56055	Aei56055	Zea mays
21	59	44.7	1336	10	AEI56065	Aei56065	Zea mays
22	59	44.7	1420	8	ADP30944	Adp30944	Human sec
23	59	44.7	1430	10	AEI56515	Aei56515	Zea mays
24	59	44.7	1549	10	AEI56141	Aei56141	Zea mays
25	59	44.7	2119	10	AEI60331	Aei60331	Bread whe
26	59	44.7	2268	10	AEI57595	Aei57595	Thale cre
27	59	44.7	2328	10	AEI57469	Aei57469	Thale cre
28	59	44.7	2514	8	ADP30727	Adp30727	Human sec
29	59	44.7	2828	8	ADP30938	Adp30938	Human sec
30	58.5	44.3	137	7	ABO80869	Abo80869	Pseudomon
31	58.5	44.3	1233	8	ADP30523	Adp30523	Human sec
32	58.5	44.3	1602	10	AEI56221	Aei56221	Zea mays
33	58	43.9	1131	10	AEI57137	Aei57137	Thale cre
34	58	43.9	1345	10	AEI57781	Aei57781	Zea mays
35	58	43.9	1806	10	AEI56405	Aei56405	Zea mays
36	58	43.9	2272	8	ADP31136	Adp31136	Human sec
37	58	43.9	2314	10	AEI57977	Aei57977	Thale cre
38	58	43.9	4659	10	AEI57349	Aei57349	Thale cre
39	57.5	43.6	994	10	AEI56451	Aei56451	Zea mays
40	57.5	43.6	1209	10	AEI57417	Aei57417	Thale cre
41	57.5	43.6	1431	10	AEI57865	Aei57865	Thale cre
42	57.5	43.6	1527	10	AEI56859	Aei56859	Thale cre
43	57.5	43.6	3426	10	AEI57085	Aei57085	Thale cre
44	57	43.2	583	8	ADP30553	Adp30553	Human sec
45	57	43.2	1067	10	AEI57251	Aei57251	Thale cre
46	57	43.2	1116	8	ADP31203	Adp31203	Human sec
47	57	43.2	1116	8	ADP31202	Adp31202	Human sec
48	57	43.2	1250	10	AEI57421	Aei57421	Thale cre
49	57	43.2	1251	10	AEI55959	Aei55959	Thale cre
50	57	43.2	1289	8	ADP30675	Adp30675	Human sec
51	57	43.2	1292	10	AEI57269	Aei57269	Thale cre
52	57	43.2	1293	10	AEI56357	Aei56357	Thale cre
53	57	43.2	1337	10	AEI55909	Aei55909	Thale cre
54	57	43.2	1413	10	AEI56187	Aei56187	Zea mays
55	57	43.2	1462	10	AEI56075	Aei56075	Zea mays
56	57	43.2	1481	8	ADP30948	Adp30948	Human sec
57	57	43.2	1486	10	AEI58055	Aei58055	Thale cre
58	57	43.2	1500	10	AEI57055	Aei57055	Thale cre
59	57	43.2	1506	8	ADP30596	Adp30596	Human sec
60	57	43.2	1509	10	AEI57371	Aei57371	Thale cre
61	57	43.2	1510	10	AEI56371	Aei56371	Thale cre
62	57	43.2	1539	8	ADP31201	Adp31201	Human sec
63	57	43.2	1539	8	ADP31200	Adp31200	Human sec

OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:06 ; Search time 69 Seconds
                                              (without alignments)
                                              163.111 Million cell updates/sec

Title: SEQ22-SEQ22
Perfect score: 126
Sequence: 1 CSKIASMETGCcskiasmetgcg 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   A_Geneseq_200701:*
                 1:   geneseqp1980s:*
                 2:   geneseqp1990s:*
                 3:   geneseqp2000s:*
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                 6:   geneseqp2003as:*
                 7:   geneseqp2003bs:*
                 8:   geneseqp2004s:*
                 9:   geneseqp2005s:*
                 10: geneseqp2006s:*
                 11: geneseqp2007s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	66	52.4	12	8	ADO85941	Ado85941 Cyclic po
2	64	50.8	3723	10	AEI58335	Aei58335 Zea mays
3	59	46.8	12	8	ADO85940	Ado85940 Cyclic po
4	57	45.2	2828	8	ADP30938	Adp30938 Human sec
5	55	43.7	51	4	ABB03442	Abb03442 Human mus
6	55	43.7	51	6	ABU12736	Abu12736 Novel hum

7	55	43.7	51	8	ADJ28762	Adj28762 Human mus
8	55	43.7	171	5	AAE18324	Aae18324 Sheep ker
9	54	42.9	174	9	AEA15441	Aea15441 Human pol
10	54	42.9	174	10	AEK59301	Aek59301 Human ker
11	54	42.9	174	10	AEL18833	Ael18833 Human ker
12	54	42.9	1509	10	AEI57371	Aei57371 Thale cre
13	54	42.9	1510	10	AEI56371	Aei56371 Thale cre
14	53	42.1	615	8	ADP30803	Adp30803 Human sec
15	53	42.1	1035	9	AED44877	Aed44877 Aurora pr
16	53	42.1	1779	10	AEI56971	Aei56971 Thale cre
17	53	42.1	2808	8	ADP31258	Adp31258 Human sec
18	53	42.1	4683	8	ADP31260	Adp31260 Human sec
19	53	42.1	4848	8	ADP31259	Adp31259 Human sec
20	52	41.3	507	8	ADP30869	Adp30869 Human sec
21	52	41.3	1215	10	AEI58333	Aei58333 Zea mays
22	52	41.3	1549	10	AEI56141	Aei56141 Zea mays
23	52	41.3	1639	10	AEI56667	Aei56667 Zea mays
24	52	41.3	1825	10	AEI56415	Aei56415 Zea mays
25	52	41.3	2101	10	AEI56311	Aei56311 Zea mays
26	52	41.3	2280	10	AEI57411	Aei57411 Thale cre
27	52	41.3	2487	10	AEI57141	Aei57141 Thale cre
28	52	41.3	2604	10	AEI57169	Aei57169 Thale cre
29	51.5	40.9	1481	10	AEI56411	Aei56411 Zea mays
30	51	40.5	753	8	ADP30988	Adp30988 Human sec
31	51	40.5	1042	10	AEI55889	Aei55889 Thale cre
32	51	40.5	1042	10	AEI58033	Aei58033 Thale cre
33	51	40.5	1071	9	AEC05688	Aec05688 Human pep
34	51	40.5	1071	10	AEH16870	Aeh16870 Human pep
35	51	40.5	1191	8	ADP30993	Adp30993 Human sec
36	51	40.5	1316	10	AEI56237	Aei56237 Zea mays
37	51	40.5	1498	8	ADP30684	Adp30684 Human sec
38	51	40.5	1815	8	ADP31601	Adp31601 Human sec
39	51	40.5	1833	8	ADP30642	Adp30642 Human sec
40	51	40.5	2598	10	AEI57021	Aei57021 Thale cre
41	50.5	40.1	396	8	ADP31625	Adp31625 Human sec
42	50.5	40.1	504	8	ADP31624	Adp31624 Human sec
43	50.5	40.1	1431	8	ADP31051	Adp31051 Human sec
44	50	39.7	252	8	ADP31487	Adp31487 Human sec
45	50	39.7	348	8	ADP31676	Adp31676 Human sec
46	50	39.7	856	8	ADP30972	Adp30972 Human sec
47	50	39.7	906	8	ADP31344	Adp31344 Human sec
48	50	39.7	1192	8	ADP31180	Adp31180 Human sec
49	50	39.7	1205	10	AEI58291	Aei58291 Thale cre
50	50	39.7	1289	8	ADP30675	Adp30675 Human sec
51	50	39.7	1302	8	ADP31695	Adp31695 Human sec
52	50	39.7	1432	10	AEI56633	Aei56633 Zea mays
53	50	39.7	1464	10	AEI56649	Aei56649 Zea mays
54	50	39.7	1568	10	AEI58079	Aei58079 Thale cre
55	50	39.7	1595	10	AEI57633	Aei57633 Thale cre
56	50	39.7	1611	10	AEI57767	Aei57767 Thale cre
57	50	39.7	1611	10	AEI58085	Aei58085 Thale cre
58	50	39.7	1638	10	AEI56193	Aei56193 Zea mays
59	50	39.7	1806	10	AEI56405	Aei56405 Zea mays
60	50	39.7	2344	10	AEI57029	Aei57029 Thale cre
61	50	39.7	3046	8	ADP31684	Adp31684 Human sec
62	50	39.7	3579	8	ADP31098	Adp31098 Human sec
63	50	39.7	4659	10	AEI57349	Aei57349 Thale cre

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:59 ; Search time 166 Seconds
                                      (without alignments)
                                      148.996 Million cell updates/sec

Title: SEQ18-SEQ18
Perfect score: 138
Sequence: 1 CSSVTAWTTGcCSSVTAWTTGcg 23

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   UniProt_8.4:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES

| | | %
Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	57	41.3	38	1	COAT3_BPPHL	P68672 bacteriopha
2	57	41.3	38	1	COAT3_XANCP	P68671 xanthomonas
3	57	41.3	38	2	Q3BSR4_XANC5	Q3bsr4 xanthomonas
4	57	41.3	38	2	Q4UUU6_XANC8	Q4uuu6 xanthomonas
5	57	41.3	647	2	Q9PT10_ONCMY	Q9pt10 oncorhynchu
6	56.5	40.9	257	1	CJ095_HUMAN	Q9h7t3 homo sapien
7	56.5	40.9	569	2	Q4QGR6_LEIMA	Q4qgr6 leishmania
8	56	40.6	965	2	Q23JG4_TETTH	Q23jg4 tetrahymena
9	54.5	39.5	725	2	Q4T771_TETNG	Q4t771 tetraodon n
10	54.5	39.5	1044	2	Q4RU50_TETNG	Q4ru50 tetraodon n
11	54	39.1	239	2	Q4S5B5_TETNG	Q4s5b5 tetraodon n
12	54	39.1	714	2	Q51753_PSEFL	Q51753 pseudomonas
13	54	39.1	2289	2	Q4S3T6_TETNG	Q4s3t6 tetraodon n
14	53.5	38.8	563	2	Q5NZ27_AZOSE	Q5nz27 azoarcus sp
15	53	38.4	291	2	Q2JH08_FRASC	Q2jh08 frankia sp.

16	53	38.4	483	2	Q4DW34_TRYCR	Q4dw34	trypanosoma
17	53	38.4	547	2	Q3TXH8_MOUSE	Q3txh8	mus musculu
18	53	38.4	757	2	Q2Z090_9GAMM	Q2z090	uncultured
19	52.5	38.0	62	2	Q6H539_ORYSA	Q6h539	oryza sativ
20	52.5	38.0	270	2	Q9LH57_ARATH	Q9lh57	arabidopsis
21	52.5	38.0	282	2	Q9C7C1_ARATH	Q9c7c1	arabidopsis
22	52.5	38.0	443	2	Q3TGD7_MOUSE	Q3tgd7	mus musculu
23	52.5	38.0	503	2	Q3TL84_MOUSE	Q3tl84	mus musculu
24	52.5	38.0	539	1	LRMP_MOUSE	Q60664	mus musculu
25	52.5	38.0	539	2	Q3TVR1_MOUSE	Q3tvr1	mus musculu
26	52.5	38.0	582	2	Q1E148_COCIM	Q1e148	coccidioide
27	52	37.7	305	1	POPD3_CHICK	Q9dg25	gallus gall
28	52	37.7	431	2	Q5GVM4_XANOR	Q5gvm4	xanthomonas
29	52	37.7	435	2	Q3JP43_BURP1	Q3jp43	burkholderi
30	52	37.7	474	2	O49335_ARATH	O49335	arabidopsis
31	52	37.7	480	2	Q8RWE3_ARATH	Q8rwe3	arabidopsis
32	52	37.7	542	2	Q235T5_TETTH	Q235t5	tetrahymena
33	52	37.7	693	2	Q9DG20_CHICK	Q9dg20	gallus gall
34	52	37.7	922	2	Q2R1X1_ORYSA	Q2r1x1	oryza sativ
35	52	37.7	1214	2	Q4P8U0_USTMA	Q4p8u0	ustilago ma
36	51.5	37.3	305	2	Q387P3_9TRYP	Q387p3	trypanosoma
37	51.5	37.3	497	2	Q947N0_ORYSA	Q947n0	oryza sativ
38	51.5	37.3	498	2	Q6K9G3_ORYSA	Q6k9g3	oryza sativ
39	51.5	37.3	797	2	Q8UW62_ORENI	Q8uw62	oreochromis
40	51	37.0	58	2	Q33B75_ORYSA	Q33b75	oryza sativ
41	51	37.0	208	2	Q5YTQ3_NOCFA	Q5ytq3	nocardia fa
42	51	37.0	220	2	Q2U0X3_ASPOR	Q2u0x3	aspergillus
43	51	37.0	484	2	Q7M3V0_LIMPO	Q7m3v0	limulus pol
44	51	37.0	618	2	Q5Z3K8_NOCFA	Q5z3k8	nocardia fa
45	51	37.0	635	2	Q6SK16_ARTAU	Q6sk16	arthrobacte
46	50.5	36.6	152	2	Q2NS34_SODGM	Q2ns34	sodalis glo
47	50.5	36.6	314	2	Q3A5M5_PELCD	Q3a5m5	pelobacter
48	50.5	36.6	327	2	Q4RES0_TETNG	Q4res0	tetraodon n
49	50.5	36.6	330	2	Q6NWF2_BRARE	Q6nwf2	brachydanio
50	50.5	36.6	594	2	Q7SHC4_NEUCR	Q7shc4	neurospora
51	50.5	36.6	2451	2	Q52R83_PHYCI	Q52r83	phytophthor
52	50.5	36.6	3067	2	Q4S7T9_TETNG	Q4s7t9	tetraodon n
53	50.5	36.6	3148	1	HD_FUGRU	P51112	fugu rubrip
54	50	36.2	80	2	Q925H8_MOUSE	Q925h8	mus musculu
55	50	36.2	148	2	O16122_TENMO	O16122	tenebrio mo
56	50	36.2	254	2	Q24NC6_DESHY	Q24nc6	desulfitoba
57	50	36.2	264	2	Q3VWM4_PROAE	Q3vwm4	prosthecoch
58	50	36.2	291	1	POPD3_HUMAN	Q9hbv1	homo sapien
59	50	36.2	291	2	Q5T3Y8_HUMAN	Q5t3y8	homo sapien
60	50	36.2	291	2	Q3BCU3_RAT	Q3bcu3	rattus norv
61	50	36.2	342	2	Q1XGM4_PSEPU	Q1xgm4	pseudomonas
62	50	36.2	413	2	Q2U6A4_ASPOR	Q2u6a4	aspergillus
63	50	36.2	526	2	Q231M5_TETTH	Q231m5	tetrahymena
64	50	36.2	528	2	Q4T959_TETNG	Q4t959	tetraodon n
65	50	36.2	739	2	Q865F2_RABIT	Q865f2	oryctolagus
66	50	36.2	854	2	Q4IPQ1_GIBZE	Q4ipq1	gibberella
67	49.5	35.9	110	2	Q7UWQ9_RHOBA	Q7uwq9	rhodopirell
68	49.5	35.9	121	2	Q7PQT7_ANOGA	Q7pqt7	anopheles g
69	49.5	35.9	157	2	Q7X094_9BACT	Q7x094	uncultured
70	49.5	35.9	202	2	Q7WAW6_BORPA	Q7waw6	bordetella
71	49.5	35.9	397	2	Q3FAQ0_9BURK	Q3faq0	burkholderi
72	49.5	35.9	513	2	Q6F5D8_CAMSI	Q6f5d8	camellia si

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:59 ; Search time 166 Seconds
                                            (without alignments)
                                            148.996 Million cell updates/sec

Title: SEQ18-SEQ22
Perfect score: 132
Sequence: 1 CSSVTAWTTGCCSKIASMETGCG 23

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   UniProt_8.4:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % | | | | |
| Result | | Query | | | | |
No.	Score	Match	Length	DB	ID	Description
1	56	42.4	58	2	Q33B75_ORYSA	Q33b75 oryza sativ
2	54	40.9	220	2	Q2U0X3_ASPOR	Q2u0x3 aspergillus
3	54	40.9	254	2	Q24NC6_DESHY	Q24nc6 desulfitoba
4	54	40.9	545	2	Q57VH9_9TRYP	Q57vh9 trypanosoma
5	53.5	40.5	484	2	Q4WE13_ASPFU	Q4we13 aspergillus
6	53.5	40.5	569	2	Q4QGR6_LEIMA	Q4qgr6 leishmania
7	53	40.2	492	2	Q8RWI7_ARATH	Q8rwi7 arabidopsis
8	53	40.2	511	2	Q9LH69_ARATH	Q9lh69 arabidopsis
9	52.5	39.8	1246	2	Q5BFY1_EMENI	Q5bfy1 emericella
10	52	39.4	597	2	Q7QSQ5_GIALA	Q7qsq5 giardia lam
11	52	39.4	865	2	Q4SZU5_TETNG	Q4szu5 tetraodon n
12	52	39.4	1251	2	Q9ZNV6_ORYSA	Q9znv6 oryza sativ
13	52	39.4	1251	2	Q9SSY0_ORYSA	Q9ssy0 oryza sativ
14	51.5	39.0	81	2	Q8N0U1_HUMAN	Q8n0u1 homo sapien
15	51.5	39.0	421	2	Q95V69_TETTH	Q95v69 tetrahymena

16	51	38.6	99	2	Q5YF48_9VIRU	Q5yf48 rock bream
17	51	38.6	214	2	Q6ZSQ4_HUMAN	Q6zsq4 homo sapien
18	51	38.6	603	2	Q9YGH6_9NEOB	Q9ygh6 rana shqipe
19	50.5	38.3	173	2	Q5DCF9_SCHJA	Q5dcf9 schistosoma
20	50.5	38.3	596	2	Q3PCG7_PARDE	Q3pcg7 paracoccus
21	50.5	38.3	797	2	Q8UW62_ORENI	Q8uw62 oreochromis
22	50	37.9	93	2	Q5MCZ1_SHEEP	Q5mcz1 ovis aries
23	50	37.9	103	2	Q5MCZ2_SHEEP	Q5mcz2 ovis aries
24	50	37.9	151	1	KRB2C_SHEEP	P02440 ovis aries
25	50	37.9	152	2	Q5MCZ8_SHEEP	Q5mcz8 ovis aries
26	50	37.9	152	2	Q5MD00_SHEEP	Q5md00 ovis aries
27	50	37.9	152	2	Q7JFW8_SHEEP	Q7jfw8 ovis aries
28	50	37.9	152	2	Q7JFX1_SHEEP	Q7jfx1 ovis aries
29	50	37.9	152	2	Q5MD03_SHEEP	Q5md03 ovis aries
30	50	37.9	152	2	Q7JFW9_SHEEP	Q7jfw9 ovis aries
31	50	37.9	171	1	KRB2A_SHEEP	P02438 ovis aries
32	50	37.9	177	2	Q5XJ63_BRARE	Q5xj63 brachydanio
33	50	37.9	182	2	Q29619_SHEEP	Q29619 ovis aries
34	50	37.9	303	2	Q2UIW2_ASPOR	Q2uiw2 aspergillus
35	50	37.9	348	2	Q26Q48_XANP2	Q26q48 xanthobacte
36	50	37.9	483	2	Q4DW34_TRYCR	Q4dw34 trypanosoma
37	49	37.1	236	2	Q4RLR8_TETNG	Q4rlr8 tetraodon n
38	49	37.1	286	2	Q8UVU5_SPAAU	Q8uvu5 sparus aura
39	49	37.1	459	2	Q4FZ07_LEIMA	Q4fz07 leishmania
40	49	37.1	491	1	K2M2_SHEEP	P15241 ovis aries
41	49	37.1	537	2	Q2HEN6_CHAGB	Q2hen6 chaetomium
42	49	37.1	734	2	Q9LNZ0_ARATH	Q9lnz0 arabidopsis
43	49	37.1	1886	2	Q7X504_9LEPT	Q7x504 leptospira
44	49	37.1	1889	2	Q7X2A1_LEPIN	Q7x2a1 leptospira
45	49	37.1	1890	2	Q72V39_LEPIC	Q72v39 leptospira
46	49	37.1	1891	2	Q8EZS3_LEPIN	Q8ezs3 leptospira
47	49	37.1	2458	2	Q4CUV0_TRYCR	Q4cuv0 trypanosoma
48	49	37.1	2731	2	Q4CV28_TRYCR	Q4cv28 trypanosoma
49	49	37.1	2771	2	Q9WTS7_MOUSE	Q9wts7 mus musculu
50	49	37.1	2796	2	Q3UHK6_MOUSE	Q3uhk6 mus musculu
51	49	37.1	2825	2	O70465_MOUSE	O70465 mus musculu
52	49	37.1	2833	2	Q3UH52_MOUSE	Q3uh52 mus musculu
53	48.5	36.7	304	2	Q2P8K4_XANOM	Q2p8k4 xanthomonas
54	48.5	36.7	307	2	Q5H5W1_XANOR	Q5h5w1 xanthomonas
55	48.5	36.7	376	2	Q59F39_HUMAN	Q59f39 homo sapien
56	48.5	36.7	620	1	ITK_HUMAN	Q08881 homo sapien
57	48.5	36.7	620	2	Q32ML7_HUMAN	Q32ml7 homo sapien
58	48.5	36.7	2262	2	Q1XSM3_CYTJO	Q1xsm3 flavobacter
59	48	36.4	83	2	Q5MCZ0_SHEEP	Q5mcz0 ovis aries
60	48	36.4	126	2	Q5C0X9_SCHJA	Q5c0x9 schistosoma
61	48	36.4	156	1	KRB2B_SHEEP	P02439 ovis aries
62	48	36.4	162	2	Q7JFX2_SHEEP	Q7jfx2 ovis aries
63	48	36.4	174	1	KRA15_HUMAN	Q9bys1 homo sapien
64	48	36.4	181	1	KRB2D_SHEEP	P08131 ovis aries
65	48	36.4	264	2	Q9ALV8_RHOSH	Q9alv8 rhodobacter
66	48	36.4	281	2	Q5TX10_ANOGA	Q5tx10 anopheles g
67	48	36.4	315	2	Q561R8_RAT	Q561r8 rattus norv
68	48	36.4	352	2	Q7ULA1_RHOBA	Q7ula1 rhodopirell
69	48	36.4	362	2	Q7QJL0_ANOGA	Q7qjl0 anopheles g
70	48	36.4	367	2	Q1YTF4_9GAMM	Q1ytf4 marine gamm
71	48	36.4	379	2	Q3HGC9_TRIER	Q3hgc9 trichodesmi
72	48	36.4	413	2	Q2U2P6_ASPOR	Q2u2p6 aspergillus

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:59 ; Search time 166 Seconds
                                              (without alignments)
                                              148.996 Million cell updates/sec

Title: SEQ22-SEQ18
Perfect score: 132
Sequence: 1 CSKIASMETGCCSSVTAWTTGCG 23

Scoring table: BLOSUM62
                  Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   UniProt_8.4:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
   No.   Score   Match Length DB   ID   Description
----
       1   55.5   42.0   2451   2   Q52R83_PHYCI   Q52r83 phytophthor
       2   55   41.7   732   2   Q6BGR5_DEBHA   Q6bgr5 debaryomyce
       3   55   41.7   780   2   Q5AK77_CANAL   Q5ak77 candida alb
       4   54   40.9   393   2   Q3JAS4_NITOC   Q3jas4 nitrosococc
       5   53   40.2   1491   2   Q4QJI2_LEIMA   Q4qji2 leishmania
       6   52   39.4   67   2   Q9TSF0_SHEEP   Q9tsf0 ovis aries
       7   52   39.4   93   2   Q5MCZ1_SHEEP   Q5mcz1 ovis aries
       8   52   39.4   103   2   Q5MCZ2_SHEEP   Q5mcz2 ovis aries
       9   52   39.4   130   1   KRA3A_SHEEP   P02443 ovis aries
      10   52   39.4   131   1   KRA3_SHEEP   P02441 ovis aries
      11   52   39.4   131   2   Q9D3H4_MOUSE   Q9d3h4 mus musculu
      12   52   39.4   132   1   KRA3_CAPHI   P02442 capra hircu
      13   52   39.4   151   1   KRB2C_SHEEP   P02440 ovis aries
      14   52   39.4   152   2   Q29620_SHEEP   Q29620 ovis aries
      15   52   39.4   152   2   Q5MCZ8_SHEEP   Q5mcz8 ovis aries

16	52	39.4	152	2	Q5MD00_SHEEP	Q5md00 ovis aries
17	52	39.4	152	2	Q7JFW8_SHEEP	Q7jfw8 ovis aries
18	52	39.4	152	2	Q7JFX1_SHEEP	Q7jfx1 ovis aries
19	52	39.4	152	2	Q5MD03_SHEEP	Q5md03 ovis aries
20	52	39.4	152	2	Q7JFW9_SHEEP	Q7jfw9 ovis aries
21	52	39.4	171	1	KRB2A_SHEEP	P02438 ovis aries
22	52	39.4	182	2	Q29619_SHEEP	Q29619 ovis aries
23	52	39.4	474	2	O49335_ARATH	O49335 arabidopsis
24	52	39.4	480	2	Q8RWE3_ARATH	Q8rwe3 arabidopsis
25	52	39.4	922	2	Q2R1X1_ORYSA	Q2r1x1 oryza sativ
26	51	38.6	83	2	Q5MCZ0_SHEEP	Q5mcz0 ovis aries
27	51	38.6	156	1	KRB2B_SHEEP	P02439 ovis aries
28	51	38.6	162	2	Q7JFX2_SHEEP	Q7jfx2 ovis aries
29	51	38.6	181	1	KRB2D_SHEEP	P08131 ovis aries
30	51	38.6	248	2	Q6TXF2_RAT	Q6txf2 rattus norv
31	51	38.6	254	2	Q24NC6_DESHY	Q24nc6 desulfitoba
32	51	38.6	428	2	Q7S3C6_NEUCR	Q7s3c6 neurospora
33	51	38.6	569	2	Q4QGR6_LEIMA	Q4qgr6 leishmania
34	51	38.6	691	2	Q3W5R7_9ACTO	Q3w5r7 frankia sp.
35	51	38.6	1825	2	Q4LVD2_9BURK	Q4lvd2 burkholderi
36	51	38.6	1825	2	Q1BQ40_9BURK	Q1bq40 burkholderi
37	51	38.6	1848	2	Q4S113_TETNG	Q4s113 tetraodon n
38	50.5	38.3	360	2	Q86AK7_DICDI	Q86ak7 dictyosteli
39	50.5	38.3	360	2	Q556S1_DICDI	Q556s1 dictyosteli
40	50.5	38.3	846	2	Q31GH1_THICR	Q31gh1 thiomicrosp
41	50	37.9	116	2	Q7TWQ5_MYCBO	Q7twq5 mycobacteri
42	50	37.9	237	2	O53144_MYCTU	O53144 mycobacteri
43	50	37.9	270	2	Q9ZUN5_ARATH	Q9zun5 arabidopsis
44	50	37.9	449	2	Q8SWZ1_DROME	Q8swz1 drosophila
45	50	37.9	500	2	Q28XK8_DROPS	Q28xk8 drosophila
46	50	37.9	618	2	Q5Z3K8_NOCFA	Q5z3k8 nocardia fa
47	50	37.9	793	2	Q5N8W8_ORYSA	Q5n8w8 oryza sativ
48	50	37.9	817	2	Q4Q251_LEIMA	Q4q251 leishmania
49	50	37.9	1186	2	Q4CXC5_TRYCR	Q4cxc5 trypanosoma
50	50	37.9	1189	2	Q4DTX2_TRYCR	Q4dtx2 trypanosoma
51	50	37.9	1809	2	O85740_PSEAE	O85740 pseudomonas
52	50	37.9	1809	2	Q9RFM7_PSEAE	Q9rfm7 pseudomonas
53	50	37.9	1809	2	Q9HWG4_PSEAE	Q9hwg4 pseudomonas
54	49.5	37.5	257	1	CJ095_HUMAN	Q9h7t3 homo sapien
55	49	37.1	78	1	M6_LILHE	Q40189 lilium henr
56	49	37.1	143	2	Q1D7P2_MYXXA	Q1d7p2 myxococcus
57	49	37.1	161	2	Q6R9B0_MAIZE	Q6r9b0 zea mays (m
58	49	37.1	227	2	Q4QSJ9_9LECA	Q4qsj9 pertusaria
59	49	37.1	249	2	Q5V9X6_MLVFR	Q5v9x6 friend muri
60	49	37.1	407	2	Q1NTQ7_9DELT	Q1ntq7 delta prote
61	49	37.1	431	2	Q5GVM4_XANOR	Q5gvm4 xanthomonas
62	49	37.1	569	2	Q2R345_ORYSA	Q2r345 oryza sativ
63	49	37.1	675	1	ENV_MLVF5	P03390 friend muri
64	49	37.1	676	2	Q7ZGR3_9GAMR	Q7zgr3 murine leuk
65	48.5	36.7	183	2	Q5JQU0_ORYSA	Q5jqu0 oryza sativ
66	48.5	36.7	370	2	Q2KJ85_BOVIN	Q2kj85 bos taurus
67	48.5	36.7	582	2	Q1E148_COCIM	Q1e148 coccidioide
68	48.5	36.7	3340	2	Q4BB2_LEIMA	Q4qbb2 leishmania
69	48	36.4	85	2	Q9BYT5_HUMAN	Q9byt5 homo sapien
70	48	36.4	96	2	Q9BYU5_HUMAN	Q9byu5 homo sapien
71	48	36.4	120	2	Q38IX3_TENMO	Q38ix3 tenebrio mo
72	48	36.4	128	1	KRA24_HUMAN	Q9byr9 homo sapien

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:59 ; Search time 166 Seconds
                                    (without alignments)
                                    148.996 Million cell updates/sec

Title: SEQ22-SEQ22
Perfect score: 126
Sequence: 1 CSKIASMETGCcskiasmetgcg 23

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues

Total number of hits satisfying chosen parameters: 3281787

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   UniProt_8.4:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                            SUMMARIES

		%				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	55	43.7	93	2	Q5MCZ1_SHEEP	Q5mcz1 ovis aries
2	55	43.7	103	2	Q5MCZ2_SHEEP	Q5mcz2 ovis aries
3	55	43.7	151	1	KRB2C_SHEEP	P02440 ovis aries
4	55	43..7	152	2	Q5MCZ8_SHEEP	Q5mcz8 ovis aries
5	55	43.7	152	2	Q5MD00_SHEEP	Q5md00 ovis aries
6	55	43.7	152	2	Q7JFW8_SHEEP	Q7jfw8 ovis aries
7	55	43.7	152	2	Q7JFX1_SHEEP	Q7jfx1 ovis aries
8	55	43.7	152	2	Q5MD03_SHEEP	Q5md03 ovis aries
9	55	43.7	152	2	Q7JFW9_SHEEP	Q7jfw9 ovis aries
10	55	43.7	171	1	KRB2A_SHEEP	P02438 ovis aries
11	55	43.7	182	2	Q29619_SHEEP	Q29619 ovis aries
12	55	43.7	254	2	Q24NC6_DESHY	Q24nc6 desulfitoba
13	54	42.9	83	2	Q5MCZ0_SHEEP	Q5mcz0 ovis aries
14	54	42.9	156	1	KRB2B_SHEEP	P02439 ovis aries
15	54	42.9	162	2	Q7JFX2_SHEEP	Q7jfx2 ovis aries

16	54	42.9	174	1	KRA15_HUMAN		Q9bys1	homo sapien
17	54	42.9	181	1	KRB2D_SHEEP		P08131	ovis aries
18	54	42.9	545	2	Q57VH9_9TRYP		Q57vh9	trypanosoma
19	52.5	41.7	512	2	Q4SAY1_TETNG		Q4say1	tetraodon n
20	52	41.3	272	2	Q3K4K1_PSEPF		Q3k4k1	pseudomonas
21	52	41.3	1848	2	Q4S113_TETNG		Q4s113	tetraodon n
22	51.5	40.9	1246	2	Q5BFY1_EMENI		Q5bfy1	emericella
23	51	40.5	152	2	Q29620_SHEEP		Q29620	ovis aries
24	51	40.5	241	2	Q2KT15_9EURO		Q2kt15	aspergillus
25	51	40.5	450	2	Q34VI7_9GAMM		Q34vi7	alkalilimni
26	51	40.5	826	2	Q5KTW4_ENTHI		Q5ktw4	entamoeba h
27	51	40.5	1056	2	Q51CG0_ENTHI		Q51cg0	entamoeba h
28	50.5	40.1	175	2	P90592_PLAVI		P90592	plasmodium
29	50.5	40.1	347	2	Q75JE6_DICDI		Q75je6	dictyosteli
30	50.5	40.1	347	2	Q55AL3_DICDI		Q55al3	dictyosteli
31	50.5	40.1	384	2	Q8I208_PLAF7		Q8i208	plasmodium
32	50.5	40.1	1103	2	Q27721_PLAFA		Q27721	plasmodium
33	50.5	40.1	1208	2	Q8I5T3_PLAF7		Q8i5t3	plasmodium
34	50.5	40.1	1228	2	Q27724_PLAFA		Q27724	plasmodium
35	50.5	40.1	1264	2	Q9U445_PLAFA		Q9u445	plasmodium
36	50.5	40.1	1280	2	Q2H8G8_CHAGB		Q2h8g8	chaetomium
37	50.5	40.1	1437	2	Q4YWJ5_PLABE		Q4ywj5	plasmodium
38	50.5	40.1	1467	2	Q7RHL5_PLAYO		Q7rhl5	plasmodium
39	50.5	40.1	1528	2	Q5CKM3_CRYHO		Q5ckm3	cryptospori
40	50.5	40.1	1528	2	Q5CQZ5_CRYPV		Q5cqz5	cryptospori
41	50.5	40.1	1528	2	Q95022_CRYPV		Q95022	cryptospori
42	50	39.7	105	2	Q9QBT8_9VIRU		Q9qbt8	potato roug
43	50	39.7	227	2	Q4QSJ9_9LECA		Q4qsj9	pertusaria
44	50	39.7	1081	2	Q1S472_MEDTR		Q1s472	medicago tr
45	50	39.7	2106	2	Q6RWD9_NECHA		Q6rwd9	nectria hae
46	49.5	39.3	1358	2	Q4UHQ8_THEAN		Q4uhq8	theileria a
47	49.5	39.3	1361	2	Q4N7V0_THEPA		Q4n7v0	theileria p
48	49	38.9	119	2	Q3EAM7_ARATH		Q3eam7	arabidopsis
49	49	38.9	172	2	Q7JFX3_SHEEP		Q7jfx3	ovis aries
50	49	38.9	177	1	KRA11_HUMAN		Q07627	homo sapien
51	49	38.9	177	1	KRA13_HUMAN		Q8iug1	homo sapien
52	49	38.9	290	2	Q9UAN3_CAEEL		Q9uan3	caenorhabdi
53	49	38.9	394	2	Q1NZ29_CAEEL		Q1nz29	caenorhabdi
54	49	38.9	459	1	NHR11_CAEEL		Q23294	caenorhabdi
55	49	38.9	459	2	Q5VKT4_CAEEL		Q5vkt4	caenorhabdi
56	49	38.9	477	2	Q511U9_ENTHI		Q511u9	entamoeba h
57	48.5	38.5	236	2	Q4RLR8_TETNG		Q4rlr8	tetraodon n
58	48.5	38.5	370	2	Q2KJ85_BOVIN		Q2kj85	bos taurus
59	48	38.1	67	2	Q9TSF0_SHEEP		Q9tsf0	ovis aries
60	48	38.1	130	1	KRA3A_SHEEP		P02443	ovis aries
61	48	38.1	131	1	KRA3_SHEEP		P02441	ovis aries
62	48	38.1	131	2	Q9D3H4_MOUSE		Q9d3h4	mus musculu
63	48	38.1	132	1	KRA3_CAPHI		P02442	capra hircu
64	48	38.1	203	2	Q6YR84_ONYPE		Q6yr84	onion yello
65	48	38.1	227	2	Q4QSF6_9LECA		Q4qsf6	pertusaria
66	48	38.1	227	2	Q4QSJ8_9LECA		Q4qsj8	pertusaria
67	48	38.1	227	2	Q4QSG0_9LECA		Q4qsg0	pertusaria
68	48	38.1	303	2	Q2UIW2_ASPOR		Q2uiw2	aspergillus
69	48	38.1	360	2	Q86AK7_DICDI		Q86ak7	dictyosteli
70	48	38.1	360	2	Q556S1_DICDI		Q556s1	dictyosteli
71	48	38.1	413	2	Q2U2P6_ASPOR		Q2u2p6	aspergillus
72	48	38.1	449	2	Q8SWZ1_DROME		Q8swz1	drosophila

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:58 ; Search time 10 Seconds
                                             (without alignments)
                                      210.761 Million cell updates/sec

Title: SEQ18-SEQ18
Perfect score: 138
Sequence: 1 CSSVTAWTTGcCSSVTAWTTGcg 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                   SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	41.3	38	2	S33484	hypothetical prote
2	52.5	38.0	539	2	I49065	lymphoid-restricte
3	52	37.7	446	2	F84711	hypothetical prote
4	51	37.0	484	2	A40774	phosphocholine-bin
5	49	35.5	269	2	AG0642	4-amino-4-deoxycho
6	49	35.5	603	2	E84744	hypothetical prote
7	48.5	35.1	342	2	T29115	hypothetical prote
8	48.5	35.1	504	2	T04529	probable ammonium
9	48	34.8	47	2	T44626	hypothetical prote
10	47	34.1	152	1	KRSHHC	keratin high-sulfu
11	47	34.1	152	2	I47111	high-sulfur wool m
12	47	34.1	152	2	I47109	high-sulfur wool m
13	47	34.1	152	2	I47108	high-sulfur wool m

14	47	34.1	152	2	I47112	high-sulfur wool m
15	47	34.1	172	1	KRSHHA	keratin high-sulfu
16	47	34.1	182	2	I47105	high-sulfur wool m
17	47	34.1	317	2	H70566	hypothetical prote
18	47	34.1	907	2	AB1885	hypothetical prote
19	46.5	33.7	129	2	JH0212	lysozyme (EC 3.2.1
20	46.5	33.7	129	2	JH0211	lysozyme (EC 3.2.1
21	46.5	33.7	912	2	G96830	hypothetical prote
22	46	33.3	55	2	E82522	hypothetical prote
23	46	33.3	443	2	JC4088	chorionic gonadotr
24	46	33.3	472	2	I57445	alkaline phosphata
25	46	33.3	829	2	T33283	hypothetical prote
26	46	33.3	1418	2	T37264	phospholipase C (E
27	46	33.3	1638	2	D87749	protein unc-73b [i
28	46	33.3	2488	2	T42739	guanine nucleotide
29	46	33.3	3436	2	S55659	tegument protein 6
30	45.5	33.0	129	2	JC2144	lysozyme (EC 3.2.1
31	45.5	33.0	424	2	T38271	conserved hypothet
32	45	32.6	110	2	S16496	hypothetical prote
33	45	32.6	156	1	KRSHHB	keratin high-sulfu
34	45	32.6	162	2	I47107	high-sulfur wool m
35	45	32.6	182	1	KRSHHD	keratin high-sulfu
36	45	32.6	284	2	A97203	2-oxoacid ferredox
37	45	32.6	587	2	A55368	transferred entry
38	45	32.6	952	2	S32954	hypothetical prote
39	45	32.6	1457	2	T14577	protein kinase Yak
40	45	32.6	1809	2	T17403	pyochelin syntheta
41	45	32.6	1809	2	C83118	pyochelin syntheta
42	45	32.6	2090	2	T30075	hypothetical prote
43	45	32.6	2533	2	T28675	alpha-51D immobili
44	45	32.6	2533	2	T28674	alpha-51D-immobili
45	45	32.6	3229	2	S27852	probable cell-surf
46	44.5	32.2	145	2	H87200	conserved hypothet
47	44.5	32.2	699	2	A36275	long-chain-fatty-a
48	44	31.9	45	1	FFYZ	fulvocin C - Myxoc
49	44	31.9	125	2	G84604	hypothetical prote
50	44	31.9	172	2	I47106	high-sulfur wool m
51	44	31.9	184	2	S74136	latex proteinase i
52	44	31.9	296	2	C81906	hypothetical prote
53	44	31.9	323	2	T51621	myb-like protein [
54	44	31.9	323	2	T51645	myb-related transc
55	44	31.9	334	2	I64220	membrane protein h
56	44	31.9	393	2	JC5275	voltage-gated pota
57	44	31.9	439	2	A36385	surface antigen se
58	44	31.9	476	2	A83235	alkaline phosphata
59	44	31.9	506	2	AF0757	probable cobyric a
60	44	31.9	509	2	E86273	hypothetical prote
61	44	31.9	567	2	A84748	hypothetical prote
62	44	31.9	647	2	B41288	vascular cell adhe
63	44	31.9	661	2	F70751	hypothetical prote
64	44	31.9	676	2	T01381	env protein - muri
65	44	31.9	739	2	A41288	vascular cell adhe
66	44	31.9	764	2	T07608	chloride channel p
67	44	31.9	810	2	S65226	probable membrane
68	44	31.9	1217	1	EGMSMG	epidermal growth f
69	44	31.9	1647	2	T32934	hypothetical prote
70	44	31.9	1820	2	A55494	latent transformin

OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:58 ; Search time 10 Seconds
                                             (without alignments)
                                             210.761 Million cell updates/sec

Title: SEQ18-SEQ22
Perfect score: 132
Sequence: 1 CSSVTAWTTGCCSKIASMETGCG 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
                     %
Result   Query
  No.   Score   Match Length DB   ID   Description
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      1   50   37.9   152   1   KRSHHC   keratin high-sulfu
      2   50   37.9   152   2   I47111   high-sulfur wool m
      3   50   37.9   152   2   I47109   high-sulfur wool m
      4   50   37.9   152   2   I47112   high-sulfur wool m
      5   50   37.9   152   2   T34649   hypothetical prote
      6   50   37.9   172   1   KRSHHA   keratin high-sulfu
      7   50   37.9   182   2   I47105   high-sulfur wool m
      8   49   37.1   491   2   S05408   keratin, type II,
      9   49   37.1   2825   2   T14271   Doc4 protein, stre
     10   48.5   36.7   620   1   S33253   protein-tyrosine k
     11   48   36.4   156   1   KRSHHB   keratin high-sulfu
     12   48   36.4   162   2   I47107   high-sulfur wool m
     13   48   36.4   182   1   KRSHHD   keratin high-sulfu

14	47	35.6	172	2	I47106		high-sulfur wool m
15	47	35.6	257	2	I38025		keratin-like prote
16	47	35.6	1103	2	JC4114		Ca2+-transporting
17	47	35.6	1528	2	T37308		ATPase homolog - C
18	46	34.8	38	2	S33484		hypothetical prote
19	46	34.8	152	2	I47108		high-sulfur wool m
20	46	34.8	349	2	I55601		Na/taurocholate co
21	46	34.8	967	2	S66852		hypothetical prote
22	46	34.8	976	2	G84587		hypothetical prote
23	46	34.8	995	2	S50358		hypothetical prote
24	46	34.8	1391	2	T20406		hypothetical prote
25	45.5	34.5	322	2	A71318		conserved hypothet
26	45	34.1	810	2	S65226		probable membrane
27	45	34.1	959	2	F87206		conserved large me
28	45	34.1	1599	2	T16210		hypothetical prote
29	45	34.1	2533	2	T28675		alpha-51D immobili
30	45	34.1	2533	2	T28674		alpha-51D-immobili
31	44	33.3	64	2	F72392		hypothetical prote
32	44	33.3	129	2	E70624		truncated probable
33	44	33.3	246	2	D46482		T-cell surface gly
34	44	33.3	246	2	T01073		T cell surface gly
35	44	33.3	314	2	B48149		epithelial glycopr
36	44	33.3	485	1	ANHU		angiotensin precur
37	44	33.3	853	2	T04600		probable beta-gala
38	44	33.3	853	2	B85429		beta-galactosidase
39	44	33.3	919	2	A42764		Ca2+-transporting
40	44	33.3	1217	1	EGMSMG		epidermal growth f
41	44	33.3	1457	2	T14577		protein kinase Yak
42	43.5	33.0	683	2	A82704		1,4-beta-cellobios
43	43	32.6	90	2	PC2138		hypothetical 90 pr
44	43	32.6	94	2	T03285		anther-specific pr
45	43	32.6	175	2	S37649		high-sulfur kerati
46	43	32.6	177	2	S37650		high-sulfur kerati
47	43	32.6	266	2	F72851		late expression fa
48	43	32.6	422	2	S58173		ketoacyl synthase
49	43	32.6	430	1	A24702		serine proteinase
50	43	32.6	567	2	T11653		hypothetical prote
51	43	32.6	686	2	S30075		ferric reductase (
52	43	32.6	1196	2	H85061		hypothetical prote
53	42.5	32.2	216	2	S05575		sporozoite antigen
54	42.5	32.2	217	2	T47175		hypothetical prote
55	42.5	32.2	475	2	G70861		hypothetical prote
56	42.5	32.2	1360	2	T33922		hypothetical prote
57	42.5	32.2	1408	2	S16148		gene serrate prote
58	42	31.8	99	2	B25439		Beejin protein - s
59	42	31.8	178	2	JC2353		gamma-crystallin M
60	42	31.8	178	2	JC2355		gamma-crystallin M
61	42	31.8	178	2	I50601		gamma-crystallin M
62	42	31.8	247	2	T40191		short chain dehydr
63	42	31.8	408	2	AC1373		conserved hypothet
64	42	31.8	422	2	S35197		hypothetical prote
65	42	31.8	495	2	A70782		probable monooxyge
66	42	31.8	504	2	T04529		probable ammonium
67	42	31.8	541	2	A87595		amine oxidase, fla
68	42	31.8	554	2	S67452		hypothetical prote
69	42	31.8	567	2	A84748		hypothetical prote
70	42	31.8	576	2	A49933		proteinase SM tran

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:58 ; Search time 10 Seconds
                                           (without alignments)
                                           210.761 Million cell updates/sec

Title: SEQ22-SEQ18
Perfect score: 132
Sequence: 1 CSKIASMETGCCSSVTAWTTGCG 23

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	52	39.4	130	1	KRSH3A	keratin high-sulfu
2	52	39.4	131	1	KRGT3M	keratin high-sulfu
3	52	39.4	131	1	KRSHA3	keratin high-sulfu
4	52	39.4	132	1	KRGT3J	keratin high-sulfu
5	52	39.4	152	1	KRSHHC	keratin high-sulfu
6	52	39.4	152	2	I47111	high-sulfur wool m
7	52	39.4	152	2	I47109	high-sulfur wool m
8	52	39.4	152	2	I47108	high-sulfur wool m
9	52	39.4	152	2	I47112	high-sulfur wool m
10	52	39.4	172	1	KRSHHA	keratin high-sulfu
11	52	39.4	182	2	I47105	high-sulfur wool m
12	52	39.4	446	2	F84711	hypothetical prote
13	51	38.6	156	1	KRSHHB	keratin high-sulfu

14	51	38.6	162	2	I47107	high-sulfur wool m
15	51	38.6	182	1	KRSHHD	keratin high-sulfu
16	50	37.9	270	2	E84578	probable senescenc
17	50	37.9	1809	2	T17403	pyochelin syntheta
18	50	37.9	1809	2	C83118	pyochelin syntheta
19	49	37.1	676	2	T01381	env protein - muri
20	48	36.4	175	2	S37649	high-sulfur kerati
21	48	36.4	676	2	S70395	env polyprotein -
22	47.5	36.0	349	2	I55601	Na/taurocholate co
23	47	35.6	591	2	I48141	acrogranin - guine
24	46.5	35.2	276	2	T52349	F-box protein FBL2
25	46	34.8	172	2	I47106	high-sulfur wool m
26	46	34.8	177	2	S37650	high-sulfur kerati
27	46	34.8	233	2	T25295	hypothetical prote
28	46	34.8	237	2	H82568	purine nucleoside
29	46	34.8	256	2	F86463	hypothetical prote
30	46	34.8	342	2	T29115	hypothetical prote
31	46	34.8	421	2	T02135	hypothetical prote
32	46	34.8	506	2	AF0757	probable cobyric a
33	46	34.8	550	2	T37325	wingless protein r
34	46	34.8	605	2	T31690	hypothetical prote
35	46	34.8	764	2	T07608	chloride channel p
36	46	34.8	1192	2	T08609	hypothetical prote
37	46	34.8	3491	2	T43231	probable 6-deoxyer
38	45.5	34.5	424	2	T38271	conserved hypothet
39	45.5	34.5	1360	2	T33922	hypothetical prote
40	45	34.1	222	2	D84520	hypothetical prote
41	45	34.1	284	2	A97203	2-oxoacid ferredox
42	45	34.1	439	2	B75487	ammonium transport
43	45	34.1	810	2	S65226	probable membrane
44	45	34.1	1558	2	C89114	protein C37C3.6a [
45	45	34.1	2167	2	T34395	hypothetical prote
46	44.5	33.7	2871	2	A55567	fibrillin I - bovi
47	44.5	33.7	2871	2	A55624	fibrillin-1 precur
48	44.5	33.7	3002	2	A47221	fibrillin 1 precur
49	44	33.3	74	2	E90799	hypothetical prote
50	44	33.3	125	2	G84604	hypothetical prote
51	44	33.3	296	2	C81906	hypothetical prote
52	44	33.3	323	2	T51621	myb-like protein [
53	44	33.3	323	2	T51645	myb-related transc
54	44	33.3	455	2	B71335	probable purine-bi
55	44	33.3	472	2	I57445	alkaline phosphata
56	44	33.3	567	2	A84748	hypothetical prote
57	43.5	33.0	329	2	T43012	conserved hypothet
58	43.5	33.0	340	2	H95349	alcohol dehydrogen
59	43.5	33.0	507	2	T50398	hypothetical serin
60	43	32.6	169	1	S18946	ultra high-sulfur
61	43	32.6	227	2	C84431	hypothetical prote
62	43	32.6	353	2	D69105	coenzyme PQQ synth
63	43	32.6	433	2	S37790	probable serine/th
64	43	32.6	596	2	E87686	succinate dehydrog
65	43	32.6	676	1	VCMVPV	env polyprotein pr
66	43	32.6	829	2	T33283	hypothetical prote
67	43	32.6	1418	2	T37264	phospholipase C (E
68	43	32.6	1786	1	MMHUB1	laminin beta-1 cha
69	43	32.6	2907	2	A57278	fibrillin-2 precur
70	43	32.6	2918	2	A54105	fibrillin-2 precur

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OM protein - protein search, using sw model

Run on: August 23, 2007, 15:29:58 ; Search time 10 Seconds
                                              (without alignments)
                                              210.761 Million cell updates/sec

Title: SEQ22-SEQ22
Perfect score: 126
Sequence: 1 CSKIASMETGCcskiasmetgcg 23

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 300 summaries

Database :   PIR_80:*
                   1: pir1:*
                   2: pir2:*
                   3: pir3:*
                   4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	55	43.7	152	1	KRSHHC	keratin high-sulfu
2	55	43.7	152	2	I47111	high-sulfur wool m
3	55	43.7	152	2	I47109	high-sulfur wool m
4	55	43.7	152	2	I47112	high-sulfur wool m
5	55	43.7	172	1	KRSHHA	keratin high-sulfu
6	55	43.7	182	2	I47105	high-sulfur wool m
7	54	42.9	156	1	KRSHHB	keratin high-sulfu
8	54	42.9	162	2	I47107	high-sulfur wool m
9	54	42.9	182	1	KRSHHD	keratin high-sulfu
10	51	40.5	152	2	I47108	high-sulfur wool m
11	50.5	40.1	1103	2	JC4114	Ca2+-transporting
12	50.5	40.1	1528	2	T37308	ATPase homolog - C
13	49	38.9	172	2	I47106	high-sulfur wool m

14	49	38.9	175	2	S37649	high-sulfur kerati
15	49	38.9	177	2	S37650	high-sulfur kerati
16	49	38.9	282	2	T27554	hypothetical prote
17	49	38.9	290	2	T43351	nuclear receptor N
18	48	38.1	99	2	B25439	Beejin protein - s
19	48	38.1	130	1	KRSH3A	keratin high-sulfu
20	48	38.1	131	1	KRGT3M	keratin high-sulfu
21	48	38.1	131	1	KRSHA3	keratin high-sulfu
22	48	38.1	132	1	KRGT3J	keratin high-sulfu
23	48	38.1	1558	2	C89114	protein C37C3.6a [
24	48	38.1	2167	2	T34395	hypothetical prote
25	47.5	37.7	349	2	I55601	Na/taurocholate co
26	47	37.3	270	2	E84578	probable senescenc
27	47	37.3	491	2	S05408	keratin, type II,
28	46.5	36.9	2825	2	T14271	Doc4 protein, stre
29	46	36.5	463	2	G83175	probable metallo-o
30	46	36.5	557	1	S76051	hypothetical prote
31	46	36.5	810	2	S65226	probable membrane
32	46	36.5	3491	2	T43231	probable 6-deoxyer
33	45.5	36.1	459	2	B36145	cobG protein - Pse
34	45	35.7	188	2	JC6547	high sulfur protei
35	45	35.7	257	2	I38025	keratin-like prote
36	45	35.7	339	2	AG1910	periplasmic solute
37	45	35.7	620	1	S33253	protein-tyrosine k
38	45	35.7	1104	2	JH0181	nitrite reductase
39	44.5	35.3	591	2	I48141	acrogranin - guine
40	44.5	35.3	919	2	A42764	Ca2+-transporting
41	44	34.9	64	2	F72392	hypothetical prote
42	44	34.9	222	2	D84520	hypothetical prote
43	44	34.9	421	2	T02135	hypothetical prote
44	44	34.9	1391	2	T20406	hypothetical prote
45	43.5	34.5	137	2	F69411	hypothetical prote
46	43.5	34.5	632	2	T04732	hypothetical prote
47	43.5	34.5	1047	2	A59246	HIRA protein - fru
48	43.5	34.5	1599	2	T16210	hypothetical prote
49	43	34.1	246	2	D46482	T-cell surface gly
50	43	34.1	246	2	T01073	T cell surface gly
51	43	34.1	267	2	T25767	hypothetical prote
52	43	34.1	344	2	S76268	probable UDP-3-O-[
53	43	34.1	567	2	T11653	hypothetical prote
54	43	34.1	781	2	F86457	unknown protein, 3
55	43	34.1	1260	2	T04440	hypothetical prote
56	42.5	33.7	60	2	S31723	metallothionein -
57	42.5	33.7	60	2	B27490	metallothionein B
58	42.5	33.7	60	2	JC2420	metallothionein -
59	42.5	33.7	61	2	JC1449	metallothionein A
60	42.5	33.7	126	2	I46489	cysteine-rich hair
61	42.5	33.7	450	2	H82495	C4-dicarboxylate t
62	42.5	33.7	475	2	G70861	hypothetical prote
63	42.5	33.7	534	2	E84590	hypothetical prote
64	42.5	33.7	559	2	A57474	extracellular matr
65	42.5	33.7	946	2	G71617	SERA antigen/papai
66	42.5	33.7	1820	2	S71853	genome polyprotein
67	42	33.3	90	2	PC2138	hypothetical 90 pr
68	42	33.3	139	2	T09878	albumin 2S storage
69	42	33.3	152	2	T34649	hypothetical prote
70	42	33.3	223	2	B38346	ultra-high-sulfur